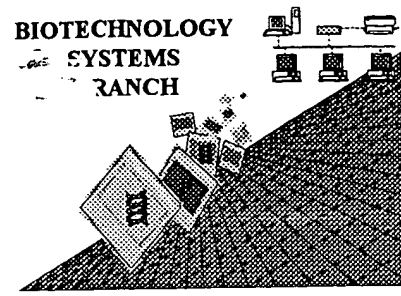


STOLE



AW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/105,117D
Unit / Team No. : 1653
Date Processed by STIC: 08/03/1999

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/105,117D

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics** The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ **Wrapped Aminos** The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ **Incorrect Line Length** The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ **Misaligned Amino Acid Numbering** The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ **Non-ASCII** This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ **Variable Length** Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ **PatentIn ver. 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 ☐ **Skipped Sequences (OLD RULES)** Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ **Skipped Sequences (NEW RULES)** Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ **Use of n's or Xaa's (NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ **Use of <213>Organism (NEW RULES)** Sequence(s) _____ are missing this mandatory field or its response.
- 12 ☐ **Use of <220>Feature (NEW RULES)** Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ **PatentIn ver. 2.0 "bug"** **Please do not use "Copy to Disk" function f PatentIn versi n 2.0.** This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

E. stole

1653

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/105,117D

DATE: 08/03/1999
TIME: 16:21:55

Input Set: I105117D.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

Does Not Comply
Corrected Diskette Needed

1 <110> APPLICANT: Vrjic, Marina
2 Eggeling, Lothar
3 Sahm, Harmann
4 <120> TITLE OF INVENTION: PROCESS FOR THE MICROBIAL PRODUCTION OF AMINO ACIDS BY
5 BOOSTED ACTIVITY OF EXPORT CARRIERS
6 <130> FILE REFERENCE: fj122 seq
7 <140> CURRENT APPLICATION NUMBER: US/09/105,117D
8 <141> CURRENT FILING DATE: 1998-06-17
9 <150> EARLIER APPLICATION NUMBER: PCT/DE96/02485
10 <151> EARLIER FILING DATE: 1996-12-18
11 <150> EARLIER APPLICATION NUMBER: 195 48 222.0
12 <151> EARLIER FILING DATE: 1995-12-22
13 <160> NUMBER OF SEQ ID NOS: 3
14 <170> SOFTWARE: PatentIn Ver. 2.0 - beta
15 <210> SEQ ID NO 1
16 <211> LENGTH: 187
17 <212> TYPE: DNA
18 <213> ORGANISM: Corynebacterium glutamicum
19 <400> SEQUENCE: 1
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22 mvrqkdvdrd dgrvdgvgr rrvsvsaggar rggwgtaamk agvddtmywr wrsrsartda 180
23 vvdagr 187
24 <210> SEQ ID NO 2
25 <211> LENGTH: 2473
26 <212> TYPE: DNA
27 <213> ORGANISM: Corynebacterium glutamicum
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32 cagttaccca tagagtagct cctcctagt gtagggacga aaatcgtaac ctgctcgaac 240
33 ccaaagccct tcttcagggg ttggttccgg agccgcttaa cggagtgggt ttggaaggcg 300
34 gctgccctgt tacctatgcg cggacgcggg gtgtcctggg agctgcgcgg gcagggtccag 360
35 tgccagaact tcgtgtagaa accctggctt cgcattctgc ccgtagcgtc ggggttagatc 420
36 aaagggtagt tggtagatcc gtagggcggt actcccccaa cgttaccggt tcaccgcgta 480
37 ccaagggtca agatgatgaa gtgtagggcg gtgcctaat cgaagtgcc aatggcgagg 540
38 attttgtaga ggtgcggcgt cgttcctatt acacacgca agtagaagg tgcgctcgca 600
39 ctgcgaacga ggtgggggtt ttgatggag caacttggtc cctcctttgg tacacctatc 660
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41 aaatcaaaga cgaacgtcgt tgtggtaaaa ggcgcgacga acgtgttcct gaagtggcg 780
42 aagccaacga aaccggccaa cccacgcgt atggttggtga gctgggtgca ctacgagctc 840
43 tcgaaattgc gcgactgagt ggcggtccccc cctttacctt tcccgattcc tccgcggaag 900
44 cttcgacgga agtagttact aactctcgtt tcacagggtca acttaccoca agtatgcctt 960

see item 10 on error
summary sheet

PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/105,117D

DATE: 08/03/1999
TIME: 16:21:55

Input Set: I105117D.RAW

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47      tcttcattac aggtctgctt ttggggggcca gtcttttact gtccatcgga ccgcagaatg 1140
48      tactgggtgat taaacaagga attaagcgcg aaggactcat tgcggttctt ctctgtgtgtt 1200
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70      gtttcctcat aga 2473

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71 <210> SEQ ID NO 3

72 <211> LENGTH: 153

73 <212> TYPE: DNA

74 <213> ORGANISM: Corynebacterium glutamicum

Item 10

75 <400> SEQUENCE: 3

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W--> 77      tvddtggsav atdtrnrvr vsvdkrvrvk mmavtwinnay davggvgayg dtgrwaagaa 120
W--> 78      aswvggaaas rskvwrwnv vvavvmtaak mmg 153

```

Input Set: I105117D.RAW

Line	?	Error/Warning	Original Text
20	W	"N" or "Xaa" used: Feature required	mndtsdgsga sasssavsrk kahhvgrvvs rtakatag
21	W	"N" or "Xaa" used: Feature required	stwnvaswg gattrdahts rrgdvjavtr anvagcvv
76	W	"N" or "Xaa" used: Feature required	mvmtggassg nvvkgkrgav vcsdvagtgv dsnaavdm
77	W	"N" or "Xaa" used: Feature required	tvddtggsav atdtrnrvrk vsvdkrvvkv mmavtwnn
78	W	"N" or "Xaa" used: Feature required	aswvggaaas rsskvwrwnv vvavvmtaak mmg